

04e0 03-09-01

OIPE

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/780,717

DATE: 03/05/2001  
 TIME: 12:46:27

Input Set : A:\Seqlist.txt  
 Output Set: N:\CRF3\03052001\I780717.raw

ENTERED

See p. 5

4 <110> APPLICANT: Helentjaris, Tim  
 5 Bates, Nic  
 6 Allen, Stephen M.  
 8 <120> TITLE OF INVENTION: Novel Invertase Inhibitors and Methods  
 9 of Use  
 11 <130> FILE REFERENCE: 035718/208677  
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/780,717  
 C--> 13 <141> CURRENT FILING DATE: 2001-02-09  
 13 <150> PRIOR APPLICATION NUMBER: US 60/181,509  
 14 <151> PRIOR FILING DATE: 2000-02-10  
 16 <160> NUMBER OF SEQ ID NOS: 54  
 18 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 20 <210> SEQ ID NO: 1  
 21 <211> LENGTH: 665  
 22 <212> TYPE: DNA  
 23 <213> ORGANISM: Zea mays  
 25 <220> FEATURE:  
 26 <221> NAME/KEY: CDS /  
 27 <222> LOCATION: (68)...(598)  
 29 <400> SEQUENCE: 1  
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 31 ggggacc'atg aag ctt ctg caa gct ctg tgc cct ctc gtc atc ctc ctc 109  
 32 Met Lys Leu Leu Gln Ala Leu Cys Pro Leu Val Ile Leu Leu  
 33 1 5 10  
 35 gcc tgc tcc acg tcc aac gct tcc gtc cta caa gac gcg tgc aag tcc 157  
 36 Ala Cys Ser Thr Ser Asn Ala Ser Val Leu Gln Asp Ala Cys Lys Ser 30  
 37 15 20 25  
 39 ttc gcc gct aag atc ccg gac acc ggc tac gcc tac tgc atc aag ttc 205  
 40 Phe Ala Ala Lys Ile Pro Asp Thr Gly Tyr Ala Tyr Cys Ile Lys Phe  
 41 35 40 45  
 43 ttc cag gcc gac agg gga agc ggc ggc gac aag cgt ggc ctc gcc 253  
 44 Phe Gln Ala Asp Arg Gly Ser Ala Gly Ala Asp Lys Arg Gly Leu Ala  
 45 50 55 60  
 47 gcc atc gcc gtg agg atc atg ggg gca gcc gcc aag agc acc gcc agt 301  
 48 Ala Ile Ala Val Arg Ile Met Gly Ala Ala Lys Ser Thr Ala Ser  
 49 65 70 75  
 51 cac atc gcc gcc ctg cgg gcc tcc gag aag gac aag gag cgg ctg gcg 349  
 52 His Ile Ala Ala Leu Arg Ala Ser Glu Lys Asp Lys Glu Arg Leu Ala  
 53 80 85 90  
 55 tgc ctc agc gat tgc tcc gag gtg tac gcg cag ggc gtg gac cag acc 397  
 56 Cys Leu Ser Asp Cys Ser Glu Val Tyr Ala Gln Ala Val Asp Gln Thr  
 57 95 100 105 110  
 59 ggc gtg gcg aag ggc atc gcc acg ccc cgg ggc cgc gcg 445  
 60 Gly Val Ala Ala Lys Gly Ile Ala Ser Gly Thr Pro Arg Gly Arg Ala  
 61 115 120 125  
 63 gac gcg gtg atg gcg ctc agc acg gtg gag gat gcc ccc ggc acc tgt  
 64 Asp Ala Val Met Ala Leu Ser Thr Val Glu Asp Ala Pro Gly Thr Cys

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65	130	135	140		541
67	gag cag ggg ttc cag gac ctg agc gtg cgt tcg ccg ctg gcc tcg gag				
68	Glu Gln Gly Phe Gln Asp Leu Ser Val Arg Ser Pro Leu Ala Ser Glu				
69	145	150	155		589
71	gac gcc ggg ttc cgg aag gat gcg tcc atc gcg ctg tct gta acg gcc				
72	Asp Ala Gly Phe Arg Lys Asp Ala Ser Ile Ala Leu Ser Val Thr Ala				
73	160	165	170		638
75	gcg ttg taa' gcaaagggtgt ataatccctt tcgatataagg taaaaatga				
76	Ala Leu *				
77	175				665
79	ataaaaaaaaaaaa aaaaaaaaaagggg cggccgc				
81	<210> SEQ ID NO: 2				
82	<211> LENGTH: 176				
83	<212> TYPE: PRT				
84	<213> ORGANISM: Zea mays				
86	<400> SEQUENCE: 2				
87	Met Lys Leu Leu Gln Ala Leu Cys Pro Leu Val Ile Leu Leu Ala Cys				
88	1 5 10 15				
89	Ser Thr Ser Asn Ala Ser Val Leu Gln Asp Ala Cys Lys Ser Phe Ala				
90	20 25 30				
91	Ala Lys Ile Pro Asp Thr Gly Tyr Ala Tyr Cys Ile Lys Phe Phe Gln				
92	35 40 45				
93	Ala Asp Arg Gly Ser Ala Gly Ala Asp Lys Arg Gly Leu Ala Ala Ile				
94	50 55 60				
95	Ala Val Arg Ile Met Gly Ala Ala Lys Ser Thr Ala Ser His Ile				
96	65 70 75 80				
97	Ala Ala Leu Arg Ala Ser Glu Lys Asp Lys Glu Arg Leu Ala Cys Leu				
98	85 90 95				
99	Ser Asp Cys Ser Glu Val Tyr Ala Gln Ala Val Asp Gln Thr Gly Val				
100	100 105 110				
101	Ala Ala Lys Gly Ile Ala Ser Gly Thr Pro Arg Gly Arg Ala Asp Ala				
102	115 120 125				
103	Val Met Ala Leu Ser Thr Val Glu Asp Ala Pro Gly Thr Cys Glu Gln				
104	130 135 140				
105	Gly Phe Gln Asp Leu Ser Val Arg Ser Pro Leu Ala Ser Glu Asp Ala				
106	145 150 155 160				
107	Gly Phe Arg Lys Asp Ala Ser Ile Ala Leu Ser Val Thr Ala Ala Leu				
108	165 170 175				
110	<210> SEQ ID NO: 3				
111	<211> LENGTH: 531				
112	<212> TYPE: DNA				
113	<213> ORGANISM: Zea mays				
115	<400> SEQUENCE: 3				
116	atgaagcttc tgcaagctct gtgccctctc gtcatcctcc tcgcctgctc cacgtccaac				60
117	gttcccgctc tacaagacgc gtcaagtcc ttccggctca agatcccgg aaccggctac				120
118	gcctactgca tcaagtcttt ccaggccgac aggggaagcg ccggcgccgaa caagcgtggc				180
119	ctcgccgcca tcgcccgtgag gatcatgggg gcagccgcca agagcaccgc cagtcacatc				240
120	gcccgcctgc gggcctccga gaaggacaag gagcggctgg cgtgcctcag cgattgcctc				300
121	gagggttacg cgcaggccgt ggaccagacc ggctgtggcgg cgaaggccat cgcctcgccc				360

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122 acgccccggg	gccgcgcgga	cgcgtgtatc	gcgttcagca	cggtggagga	tgcggccggc	420	
123 acctgtgagc	aggggttcca	ggacctgagc	gtgcgttcgc	cgctggcgc	ggaggacgcc	480	
124 ggggtccgga	aggatgcgtc	catcgcgctg	tctgttaacgg	ccgcgttata	a	531	
126 <210> SEQ ID NO: 4							
127 <211> LENGTH: 981							
128 <212> TYPE: DNA							
129 <213> ORGANISM: Zea mays							
131 <220> FEATURE:							
132 <221> NAME/KEY: CDS							
133 <222> LOCATION: (58)...(723)							
135 <400> SEQUENCE: 4							
136 gaattcggca	cgagcatctgt	ccacacaaac	acatcctact	ctcttagca	aaaagac	atg	60
137						Met	
138						1	
140 gca acc acc aag agg aag gtc atc ctc gtc ctg ttc tcc ctg							108
141 Ala Thr Lys Arg Glu Lys Val Ile Leu Val Leu Leu Phe Ser Leu							
142 5	10	15					
144 acg atg ctc cct ctc agc acc ctc ggc acc cgc tcc ggc ccg ggc							156
145 Thr Met Leu Pro Leu Ser Thr Leu Gly Thr Arg Ser Gly Pro Ala Ala							
146 20	25	30					
148 gtg cag cac cac ggc cac ggc acc acc aag cac ccc tcg cct cct							204
149 Val Gln His His Gly Gly Thr Thr Lys His Pro Ser Pro Pro							
150 35	40	45					
152 tca cca gcc acg gcg gcg ctg gta cgc agc acg tgt aac tcc acg gcg							252
153 Ser Pro Ala Thr Ala Ala Leu Val Arg Ser Thr Cys Asn Ser Thr Ala							
154 50	55	60	65				
156 tac tac gac gtg tgc gtg tcc ggc ctg ggc gac ccg tcc agc gcc							300
157 Tyr Tyr Asp Val Cys Val Ser Ala Leu Gly Ala Asp Pro Ser Ser Ala							
158 70	75	80					
160 acc gcc gac gtc cgc ggg ctc tcg acc atc gcc gtg tcc ggc ggc							348
161 Thr Ala Asp Val Arg Gly Leu Ser Thr Ile Ala Val Ser Ala Ala							
162 85	90	95					
164 gcc aac gcc tcg ggc ggc gcc acg gcc ggc gcg ctc gcc aac ggc							396
165 Ala Asn Ala Ser Gly Gly Ala Ala Thr Ala Ala Leu Ala Asn Gly							
166 100	105	110					
168 acc ggc acc gcg tcg tcg tcc aac gcg cag ggc gcc cct gcc acg gcc							444
169 Thr Gly Thr Ala Ser Ser Asn Ala Gln Ala Ala Pro Ala Thr Ala							
170 115	120	125					
172 tcc gcc gcc gcg gcg ctg ctc cgc acg tgc gca gcc aag tac ggc cag							492
173 Ser Ala Ala Ala Leu Leu Arg Thr Cys Ala Ala Lys Tyr Gly Gln							
174 130	135	140	145				
176 gcc cgg gac gcg ctg gcc gcc ggg gac tcc atc gcg cag cag gac							540
177 Ala Arg Asp Ala Leu Ala Ala Gly Asp Ser Ile Ala Gln Gln Asp							
178 150	155	160					
180 tac gac gtg gcg tcc gtg cac gtg agc gcc gcc gag tac ccg cag							588
181 Tyr Asp Val Ala Ser Val His Val Ser Ala Ala Glu Tyr Pro Gln							
182 165	170	175					
184 gtg tgt agg gtg ctg ttc cgg cgg cag aag ccc ggg cag tac ccc gcg							636
185 Val Cys Arg Val Leu Phe Arg Arg Gln Lys Pro Gly Gln Tyr Pro Ala							

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186	180	185	190		684
188	gag ctg gcg gcg agg gag gag acg ctc agg cag ctc tgc tcc gtc gcg				
189	Glu Leu Ala Ala Arg Glu Glu Thr Leu Arg Gln Leu Cys Ser Val Ala				
190	195	200	205		733
192	ctc gac atc atc ggg ctc gcc tcc acc aac acc aac taa	taagctagca			
193	Leu Asp Ile Ile Gly Leu Ala Ser Thr Asn Thr Asn	*			
194	210	215	220		793
196	gcagtggcgt ggcggcgaga aaagagagga agattaaaaaa aaagtagcac ctttttcttt				853
197	tttgttaat tactgtacgt attatattaa tttagcaggc acatgcacgc agatgcata				913
198	ttaaattata aaaaggttgg tgtgcctgcc caatcaccgt ttgaagaatt atttgagcag				973
199	cttaaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa				981
200	aactcgag				
202	<210> SEQ ID NO: 5				
203	<211> LENGTH: 221				
204	<212> TYPE: PRT				
205	<213> ORGANISM: Zea mays				
207	<400> SEQUENCE: 5				
208	Met Ala Thr Thr Lys Arg Glu Lys Val Ile Leu Val Leu Leu Phe Ser				
209	1	5	10	15	
210	Leu Thr Met Leu Pro Leu Ser Thr Leu Gly Thr Arg Ser Gly Pro Ala				
211	20	25	30		
212	Ala Val Gln His His Gly His Gly Thr Thr Lys His Pro Ser Pro				
213	35	40	45		
214	Pro Ser Pro Ala Thr Ala Ala Leu Val Arg Ser Thr Cys Asn Ser Thr				
215	50	55	60		
216	Ala Tyr Tyr Asp Val Cys Val Ser Ala Leu Gly Ala Asp Pro Ser Ser				
217	65	70	75	80	
218	Ala Thr Ala Asp Val Arg Gly Leu Ser Thr Ile Ala Val Ser Ala Ala				
219	85	90	95		
220	Ala Ala Asn Ala Ser Gly Gly Ala Ala Thr Ala Ala Leu Ala Asn				
221	100	105	110		
222	Gly Thr Gly Thr Ala Ser Ser Ser Asn Ala Gln Ala Ala Pro Ala Thr				
223	115	120	125		
224	Ala Ser Ala Ala Ala Leu Leu Arg Thr Cys Ala Ala Lys Tyr Gly				
225	130	135	140		
226	Gln Ala Arg Asp Ala Leu Ala Ala Gly Asp Ser Ile Ala Gln Gln				
227	145	150	155	160	
228	Asp Tyr Asp Val Ala Ser Val His Val Ser Ala Ala Glu Tyr Pro				
229	165	170	175		
230	Gln Val Cys Arg Val Leu Phe Arg Arg Gln Lys Pro Gly Gln Tyr Pro				
231	180	185	190		
232	Ala Glu Leu Ala Ala Arg Glu Glu Thr Leu Arg Gln Leu Cys Ser Val				
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234	Ala Leu Asp Ile Ile Gly Leu Ala Ser Thr Asn Thr Asn				
235	210	215	220		
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238	<211> LENGTH: 666				
239	<212> TYPE: DNA				
240	<213> ORGANISM: Zea mays				

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242 <400> SEQUENCE: 6		60
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244 cctctcagca ccctccggac ccgcctccggc cccggggcccg tgcagcacca cggccacggc		180
245 ggcaccacca agcacccctc gcctccctca ccagccacgg cggcgcttgtt acgcagcagc		240
246 tctaactcca cggcgtaacta cgacgtgtgc gtgtccggc tggggccggc cccgtccagc		300
247 gccaccggcg acgtccggc gctctcgacc atcggcgatgtt ccggcgccggc cgccaaacgcc		360
248 tcggggccggc cggccacggc cggcgccggc gecgcgtggc gctgtcccg cacgtgcgca		420
249 aacgcgcagg cggcccccgc caegcetcc gecgcgtggc gggactccat cgccgcagcag		480
250 gccaagtacg gccaggcccg ggacgcgtg gccgcggccgg agtacccgca ggtgtgttagg		540
251 gactacgacy tggcgctcgt gcacgtgagc gccgcggccgg agtacccgca ggtgtgttagg		600
252 gtgctgttcc ggcggcagaa gcccggcag taccggccgg agtggggccg gagggaggag		660
253 acgctcaggc agctctgctc cgtcgccgtc gacatcatcg ggctcgccctc caccacacc		666
254 aactaa		
256 <210> SEQ ID NO: 7		
257 <211> LENGTH: 779		
258 <212> TYPE: DNA		
259 <213> ORGANISM: Vitis L		
261 <220> FEATURE:		
262 <221> NAME/KEY: CDS		
263 <222> LOCATION: (6)...(644)		
265 <400> SEQUENCE: 7		50
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267 Met Glu Ser Phe Thr Cys Leu Lys Leu Ser Ser Arg Gly Leu		
268 1 5 10 15		98
270 gca gct att gtt gtc ctc ttc ttc tac ctc tca ctc aca aca cca		
271 Ala Ala Ile Val Ala Leu Phe Phe Tyr Leu Ser Leu Thr Pro		
272 20 25 30 35		146
274 tgc tcg gcg gcc tca cca gag ccc cat ccc cct acc aat act aca caa		
275 Cys Ser Ala Ala Ser Pro Glu Pro His Pro Pro Thr Asn Thr Gln		
276 35 40 45 50		194
278 ttc atc aga acc tca tgc gga gtg act atg tac cct aag cta tgc ttc		
279 Phe Ile Arg Thr Ser Cys Gly Val Thr Met Tyr Pro Lys Leu Cys Phe		
280 55 60 65 70		242
282 aaa acc ctc tcg gct tat gcc agc acc atc caa aca agc cat atg gag		
283 Lys Thr Leu Ser Ala Tyr Ala Ser Thr Ile Gln Thr Ser His Met Glu		
284 65 70 75 80		290
286 ttg gcc aat gca gcc ctc tgt gtg agc cta aag ggc gct caa tcc tct		
287 Leu Ala Asn Ala Ala Leu Cys Val Ser Leu Lys Gly Ala Gln Ser Ser		
288 85 90 95 100		338
290 tca aac aag gta ctg aag tta tca aaa ggg cag ggg cta agc cgt aga		
291 Ser Asn Lys Val Leu Lys Leu Ser Lys Gly Gln Gly Leu Ser Arg Arg		
292 105 110 115 120		386
294 gaa gcc gca gcg ata acg gat tgc att gag aac atg cag gac tcg gtg		
295 Glu Ala Ala Ala Ile Thr Asp Cys Ile Glu Asn Met Gln Asp Ser Val		
296 115 120 125 130		434
298 gat gag ctc caa caa tct ctg gtg gcg atg aag gac ctt caa ggg cct		
299 Asp Glu Leu Gln Gln Ser Leu Val Ala Met Lys Asp Leu Gln Gly Pro		
300 130 135 140		482
302 gat ttt caa atg aaa atg agt gat ata gtg aca tgg gtg agt gca gct		

(F.Y.)

VERIFICATION SUMMARY  
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L:13 M:270 C: Current Application Number differs, Replaced Current Application No  
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:549 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13  
L:1592 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40